

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/672,282A  
Source: 1FW/6  
Date Processed by STIC: 12/4/06

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 12/04/2006

PATENT APPLICATION: US/10/672,282A

TIME: 09:52:40

Input Set : A:\SEQLIST.TXT

Output Set: N:\CRF4\12042006\J672282A.raw

3 <110> APPLICANT: Rogers, Elizabeth  
 5 <120> TITLE OF INVENTION: ISOLATED FERRIC REDUCTASE DEFECTIVE POLYPEPTIDES AND USES  
 THEREOF  
 7 <130> FILE REFERENCE: DCI-111  
 9 <140> CURRENT APPLICATION NUMBER: 10/672,282A  
 10 <141> CURRENT FILING DATE: 2003-09-25  
 12 <150> PRIOR APPLICATION NUMBER: PCT/US02/09962  
 13 <151> PRIOR FILING DATE: 2002-03-27  
 15 <160> NUMBER OF SEQ ID NOS: 20  
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
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 22 <213> ORGANISM: Arabidopsis thaliana  
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 28 aaataatccc ctctaaactc tcctagatac tcaactcatca ctactcatct caagttcacg 240  
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 30 agttctatga tttttcttag tattgcatat atgttctcta tcctactagg atatatcaac 360  
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 32 agttaactag attacgagta agaatgcaat tgtaaagcct ttttaattgaa cttcttcttc 480  
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 34 aactaagtca tacatgttga gagtagtgag agagttaagc aaaagcttaa tctagtcctt 600  
 35 ttaaaagcta acaaacatag tagagattat aagatgtttg gtgtaaataa caacaatacc 660  
 36 cagtttgtac atgtgttttag aaaatagttt ggattatggg taaaaatata taaattataa 720  
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 38 taccatgta aaaaaacaga acattagttg ttaagtttat aggtttattt tctacattaa 840  
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54 atacaaaaaa aaactaatat attaatlgag cggacggaat ttttttccaa aatcccgatg 1800
55 tgtaaatatg agaacgtttc gaggataact tacaaattaa acattaataa aaatgataaa 1860
56 gtgtagttag gagctaaatt gtgatagtaa acatctatct ctaatattat taaatgaatt 1920
57 ataatactat tttaatcata gtattaaatt tctttaatta aaaatataaa taatttcaat 1980
58 ttaattctat accaaattaa cccgaaaata ttttatctaa catacacaaa gacacataaa 2040
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60 ataaaataac attatttgtc aactagttaa ttccaattac gcaaatgat tcactttttt 2160
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63 aagactcttt atctttcacg agtaaaagtt cagcaaaacc atattttcct attgattaaa 2340
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126 &lt;212&gt; TYPE: DNA

127 &lt;213&gt; ORGANISM: Arabidopsis thaliana

129 &lt;220&gt; FEATURE:

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131 &lt;222&gt; LOCATION: (118)...(1695)

133 &lt;400&gt; SEQUENCE: 2

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136 Met
137 1
139 acg gaa act ggt gat gat ctt gct acg gtg aag aag cca atc cca ttt 168
140 Thr Glu Thr Gly Asp Asp Leu Ala Thr Val Lys Lys Pro Ile Pro Phe
141 5 10 15
143 ctc gtt atc ttc aaa gat tta aga cat gta ttc agt agg gac aca act 216
144 Leu Val Ile Phe Lys Asp Leu Arg His Val Phe Ser Arg Asp Thr Thr
145 20 25 30
147 ggg cga gag att cta ggc atc gcg ttt cca gca gct ttg gct tta gct 264
148 Gly Arg Glu Ile Leu Gly Ile Ala Phe Pro Ala Ala Leu Ala Leu Ala
149 35 40 45
151 gct gat cca atc gat tct ctg att gat acc gct ttt gtc ggg cgt tta 312
152 Ala Asp Pro Ile Asp Ser Leu Ile Asp Thr Ala Phe Val Gly Arg Leu
153 50 55 60 65
155 gga gcg gtt cag cta gcg gcg gtt gga gtt tcc att gcc ata ttc aat 360
156 Gly Ala Val Gln Leu Ala Ala Val Gly Val Ser Ile Ala Ile Phe Asn
157 70 75 80
159 caa gct tct aga att acg ata ttc cca ctt gtg agc ctc aca act tca 408
160 Gln Ala Ser Arg Ile Thr Ile Phe Pro Leu Val Ser Leu Thr Thr Ser
161 85 90 95
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168	Lys	Ala	Asn	Leu	Val	His	Ala	Glu	Thr	Ile	Leu	Val	Gln	Asp	Ser	Leu	
169		115					120					125					
171	gaa	aag	ggc	att	tct	tca	cct	aca	agt	aac	gat	acc	aac	cag	cca	cag	552
172	Glu	Lys	Gly	Ile	Ser	Ser	Pro	Thr	Ser	Asn	Asp	Thr	Asn	Gln	Pro	Gln	
173	130						135					140				145	
175	caa	cct	cca	gct	ccg	gat	aca	aag	tca	aat	agc	gga	aac	aaa	tcg	aat	600
176	Gln	Pro	Pro	Ala	Pro	Asp	Thr	Lys	Ser	Asn	Ser	Gly	Asn	Lys	Ser	Asn	
177				150						155					160		
179	aaa	aag	gag	aag	agg	acc	att	aga	aca	gca	tca	aca	gct	atg	atc	ttg	648
180	Lys	Lys	Glu	Lys	Arg	Thr	Ile	Arg	Thr	Ala	Ser	Thr	Ala	Met	Ile	Leu	
181			165					170					175				
183	ggg	tta	atc	ctt	ggc	ctt	gtg	caa	gct	att	ttc	ttg	att	ttc	agt	tca	696
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185		180					185					190					
187	aag	ttg	ctt	cta	ggc	gtc	atg	gga	gtg	aaa	cca	aat	tca	cca	atg	tta	744
188	Lys	Leu	Leu	Leu	Gly	Val	Met	Gly	Val	Lys	Pro	Asn	Ser	Pro	Met	Leu	
189		195					200					205					
191	tca	cca	gca	cac	aag	tac	ttg	agc	ata	cga	gct	ttg	ggg	gct	cct	gca	792
192	Ser	Pro	Ala	His	Lys	Tyr	Leu	Ser	Ile	Arg	Ala	Leu	Gly	Ala	Pro	Ala	
193	210				215						220				225		
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196	Leu	Leu	Leu	Ser	Leu	Ala	Met	Gln	Gly	Ile	Phe	Arg	Gly	Phe	Lys	Asp	
197			230					235					240				
199	acc	aaa	act	cct	ctc	ttt	gcc	act	gtc	gta	gca	gat	gtt	atc	aac	ata	888
200	Thr	Lys	Thr	Pro	Leu	Phe	Ala	Thr	Val	Val	Ala	Asp	Val	Ile	Asn	Ile	
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203	gtt	ctc	gac	ccc	atc	ttc	att	ttt	gtg	ctt	cgt	cta	ggg	atc	atc	ggt	936
204	Val	Leu	Asp	Pro	Ile	Phe	Ile	Phe	Val	Leu	Arg	Leu	Gly	Ile	Ile	Gly	
205		260					265					270					
207	gca	gcc	att	gcc	cat	gtc	att	tct	cag	tac	ttc	atg	act	cta	ata	ttg	984
208	Ala	Ala	Ile	Ala	His	Val	Ile	Ser	Gln	Tyr	Phe	Met	Thr	Leu	Ile	Leu	
209		275				280						285					
211	ttc	gtc	ttc	ctc	gca	aag	aaa	gtt	aat	ttg	att	cca	cca	aac	ttc	ggg	1032
212	Phe	Val	Phe	Leu	Ala	Lys	Lys	Val	Asn	Leu	Ile	Pro	Pro	Asn	Phe	Gly	
213	290				295					300					305		
215	gat	ttg	cag	ttt	gga	agg	ttc	ctt	aaa	aat	ggg	cta	cta	ttg	ctg	gcg	1080
216	Asp	Leu	Gln	Phe	Gly	Arg	Phe	Leu	Lys	Asn	Gly	Leu	Leu	Leu	Leu	Ala	
217			310					315					320				
219	agg	acc	ata	gca	gtg	acg	ttt	tgt	cag	acc	tta	gca	gca	gca	atg	gcg	1128
220	Arg	Thr	Ile	Ala	Val	Thr	Phe	Cys	Gln	Thr	Leu	Ala	Ala	Ala	Met	Ala	
221			325					330					335				
223	gcg	cgg	ctg	ggt	aca	aca	cca	atg	gct	gct	ttt	cag	att	tgt	tta	caa	1176
224	Ala	Arg	Leu	Gly	Thr	Thr	Pro	Met	Ala	Ala	Phe	Gln	Ile	Cys	Leu	Gln	
225		340					345					350					
227	gta	tgg	tta	act	tct	tct	ctt	ctc	aat	gat	ggt	ctt	gcc	gtt	gct	ggt	1224
228	Val	Trp	Leu	Thr	Ser	Ser	Leu	Leu	Asn	Asp	Gly	Leu	Ala	Val	Ala	Gly	

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233 370      375      380      385
235 act gct gtt gca tcc cgt gtt cta cag atg ggt ttt gtg tta gga ctt 1320
236 Thr Ala Val Ala Ser Arg Val Leu Gln Met Gly Phe Val Leu Gly Leu
237      390      395      400
239 gga ctg tcc gtt ttt gtt gga cta ggt ctc tac ttt ggt gcc gga gtt 1368
240 Gly Leu Ser Val Phe Val Gly Leu Gly Leu Tyr Phe Gly Ala Gly Val
241      405      410      415
243 ttc tcc aag gac cct gct gtt att cac ctc atg gcc atc gga ata ccg 1416
244 Phe Ser Lys Asp Pro Ala Val Ile His Leu Met Ala Ile Gly Ile Pro
245      420      425      430
247 ttt ata gca gca acg cag cca ata aac tct ctc gcc ttt gta ttg gat 1464
248 Phe Ile Ala Ala Thr Gln Pro Ile Asn Ser Leu Ala Phe Val Leu Asp
249      435      440      445
251 gga gtc aat ttt gga gca tct gat ttt gct tac act gca tac tcc atg 1512
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253 450      455      460      465
255 gtg gga gtg gcg gcc ata agc att gca gca gta ata tat atg gca aag 1560
256 Val Gly Val Ala Ala Ile Ser Ile Ala Ala Val Ile Tyr Met Ala Lys
257      470      475      480
259 acc aat ggt ttc ata gga ata tgg ata gct ctt aca atc tat atg gct 1608
260 Thr Asn Gly Phe Ile Gly Ile Trp Ile Ala Leu Thr Ile Tyr Met Ala
261      485      490      495
263 ctc cgg gct att act gga att gcc agg atg gcg aca gga act gga ccg 1656
264 Leu Arg Ala Ile Thr Gly Ile Ala Arg Met Ala Thr Gly Thr Gly Pro
265      500      505      510
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268 Trp Arg Phe Leu Arg Gly Arg Ser Ser Ser Ser Ser Ser
269      515      520      525
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276 <211> LENGTH: 526
277 <212> TYPE: PRT
278 <213> ORGANISM: Arabidopsis thaliana
280 <400> SEQUENCE: 3
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284      20      25      30
285 Thr Gly Arg Glu Ile Leu Gly Ile Ala Phe Pro Ala Ala Leu Ala Leu
286      35      40      45
287 Ala Ala Asp Pro Ile Asp Ser Leu Ile Asp Thr Ala Phe Val Gly Arg
288      50      55      60
289 Leu Gly Ala Val Gln Leu Ala Ala Val Gly Val Ser Ile Ala Ile Phe
290 65      70      75      80

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